AMENDMENTS TO THE SPECIFICATION:

Please replace paragraph [0001] with the following amended paragraph:

[0001] This application is a continuation of Application Serial No. 09/297,535 filed October 12, 1999, now U.S. Patent No. [_____] 6,268,199, which was the National Stage of International Application No. PCT/NL97/00593 filed October 29, 1997.

Please replace paragraph [0050] with the following amended paragraph:

[0050] Modern recombinant DNA technology allows us to analyze and modify genomes at the molecular level and thus gain deeper insight into their organization and expression. In the case of RNA viruses, this requires the generation of genome-length cDNA clones from which infectious transcripts can be synthesized. In most instances, a prerequisite for the construction of infectious clones is the identification of the sequences at the termini of the respective viral genome which are probably crucial for replication of viral RNA. In a previous study, it was shown that LV contains a poly(A)tail at the 3' end (Meulenberg et al., 1993a). In the present work, the exact 5' end of the LV genome was determined. Whereas several methods have been described to determine the 5' end of viral genomic RNAs or mRNAs, but most of them have important limitations. For flaviruses and pestiviruses, a method has been used which is based on the circularization of genomic RNA. However, this method needs accompanying analyses to define the border between the 5' and 3' end of the genome. The 5' rapid amplification of cDNA ends (5' RACE) method is based on the addition of a homopolymeric tail with terminal deoxyribonucleotide transferase (TdT) to the first strand cDNA strand. However, the tailing reaction is rather inefficient and this method also requires additional analyses since it can not be concluded whether the first nucleotide of the tail represents the viral sequence or is already part of the enzymatically added tail. As described above, we have determined the utmost 5' end of the viral genome by ligation of an oligonucleotide with a specified sequence to a first strand primer extension product and

amplification by PCR. An extension of 10 nucleotides (ATGATGTGTA) (~~SEQ ID NO: 19~~ SEQ ID NO:18) with respect to the published sequence was found in several independent clones and were therefore assumed to represent the utmost 5' end nucleotides of the viral genome. Altogether, this results in a leader sequence of 221 nucleotides, which is similar in length to the leader of EAV (207 nucleotides; den Boon et al., 1991), SHFV (208 nucleotides; Zeng et al., 1995), but longer than the leader of LDV (155 nucleotides; Chen et al., 1994). However, no significant homology exists between the leader sequences of these arteriviruses.